

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/381,747
Source: 1 FW/b
Date Processed by STIC: 10/18/06

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IFW16

RAW SEQUENCE LISTING

DATE: 10/18/2006

PATENT APPLICATION: US/09/381,747

TIME: 09:07:04

Input Set : F:\UTSC550.APP.txt

Output Set: N:\CRF4\10182006\I381747.raw

3 <110> APPLICANT: TORMO, MAR
 4 TARI, ANA M.
 5 LOPEZ-BERESTEIN, GABRIEL
 6 MCDONNELL, TIMOTHY J.
 8 <120> TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY LIPOSOMAL
 9 ANTISENSE OLIGODEOXYNUCLEOTIDES
 11 <130> FILE REFERENCE: UTSC:550US
 13 <140> CURRENT APPLICATION NUMBER: 09/381,747
 C--> 14 <141> **CURRENT FILING DATE: 1999-09-22**
 16 <150> PRIOR APPLICATION NUMBER: 08/726,211
 17 <151> PRIOR FILING DATE: 1996-10-04
 19 <160> NUMBER OF SEQ ID NOS: 7
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 18
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 30 Primer
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 36 <210> SEQ ID NO: 2
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 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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 52 <213> ORGANISM: Artificial Sequence
 54 <220> FEATURE:
 55 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 56 Primer
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 62 <210> SEQ ID NO: 4
 63 <211> LENGTH: 5086
 64 <212> TYPE: DNA

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76 tccctgcccgc cggccgcgcgc cgcctgcgcgc gaactgcgcgc acgggagggt cgggaggcga 180
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82 atccttttta ggaaaagagg gaaaaataaa aaccctcccc caccacctcc ttctccccac 360
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121 Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn
122 1 5 10
124 cgg gag ata gtg atg aag tac atc cat tat aag ctg tcg cag agg ggc 1539
125 Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly
126 15 20 25
128 tac gag tgg gat gcg gga gat gtg ggc gcc gcg ccc ccg ggg gcc gcc 1587
129 Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala
130 30 35 40
132 ccc gca ccg ggc atc ttc tcc tcc cag ccc ggg cac acg ccc cat cca 1635
133 Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro
134 45 50 55
136 gcc gca tcc cgc gac ccg gtc gcc agg acc tcg ccg ctg cag acc ccg 1683
137 Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro
138 60 65 70 75
140 gct gcc ccc ggc gcc gcc gcg ggg cct gcg ctc agc ccg gtg cca cct 1731
141 Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro
142 80 85 90
144 gtg gtc cac ctg gcc ctc cgc caa gcc ggc gac gac ttc tcc cgc cgc 1779
145 Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg

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148 tac cgc ggc gac ttc gcc gag atg tcc agc cag ctg cac ctg acg ccc 1827
149 Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro
150          110          115          120
152 ttc acc gcg cgg gga cgc ttt gcc acg gtg gtg gag gag ctc ttc agg 1875
153 Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg
154          125          130          135
156 gac ggg gtg aac tgg ggg agg att gtg gcc ttc ttt gag ttc ggt ggg 1923
157 Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly
158 140          145          150          155
160 gtc atg tgt gtg gag agc gtc aac cgg gag atg tcg ccc ctg gtg gac 1971
161 Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp
162          160          165          170
164 aac atc gcc ctg tgg atg act gag tac ctg aac cgg cac ctg cac acc 2019
165 Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr
166          175          180          185
168 tgg atc cag gat aac gga ggc tgg gat gcc ttt gtg gaa ctg tac ggc 2067
169 Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly
170          190          195          200
172 ccc agc atg cgg cct ctg ttt gat ttc tcc tgg ctg tct ctg aag act 2115
173 Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr
174          205          210          215
176 ctg ctc agt ttg gcc ctg gtg gga gct tgc atc acc ctg ggt gcc tat 2163
177 Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr
178 220          225          230          235
180 ctg agc cac aag tgaagtcaac atgcctgccc caaacaata tgcaaaaggt 2215
181 Leu Ser His Lys
183 tcactaaagc agtagaata atatgcattg tcagtgatgt accatgaaac aaagctgcag 2275
185 gctgtttaag aaaaaataac acacatataa acatcacaca cacagacaga cacacacaca 2335
187 cacaacaatt aacagtcttc aggcaaaacg tcgaatcagc tattttactgc caaagggaaa 2395
189 tatcatttat tttttacatt attaagaaaa aagatttatt tatttaagac agtcccatca 2455
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231 aacattatct tgtcactgta gtttggtttt atttgaaaac ctgacaaaaa aaaagttcca 3715
233 ggtgtggaat atgggggtta tctgtacatc ctggggcatt aaaaaaaaaa caatggtggg 3775
235 gaactataaa gaagtaacaa aagaagtgac atcttcagca aataaactag gaaatttttt 3835
237 tttcttccag tttagaatca gccttgaaac attgatggaa taactctgtg gcattattgc 3895
239 attatatacc atttatctgt attaactttg gaatgtactc tgttcaatgt ttaatgctgt 3955
241 ggttgatatt tcgaaaagctg ctttaaaaaa atacatgcat ctcagcgttt ttttggtttt 4015
243 aattgtattt agttatggcc tatacactat ttgtgagcaa aggtgatcgt tttctgtttg 4075
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261 gaaacctgtg gtatgaagcc agacctccc ggcgggcctc agggaacaga atgatcagac 4615
263 ctttgaatga ttctaatttt taagcaaaat attattttat gaaagggtta cattgtcaaa 4675
265 gtgatgaata tggaatatcc aatcctgtgc tgcatacctg ccaaaatcat tttaatggag 4735
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275 cttggcccca gaactgtaca gtattgtggc tgcacttgct ctaagagtag ttgatgttgc 5035
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280 <210> SEQ ID NO: 5

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282 <212> TYPE: PRT

283 <213> ORGANISM: Homo sapiens

285 <400> SEQUENCE: 5

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290           20           25           30
292 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
293           35           40           45
295 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
296           50           55           60
298 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
299           65           70           75           80
301 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
302           85           90           95
304 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
305           100          105          110
307 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
308           115          120          125
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319 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
320          180          185          190
322 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
323          195          200          205
325 Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
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340 <222> LOCATION: (147)..(761)
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347 ccccggttgc ttttctctcg ggaagg atg gcg cac gct ggg aga acg ggg tac 173
348          Met Ala His Ala Gly Arg Thr Gly Tyr
349          1          5
351 gac aac cgg gag ata gtg atg aag tac atc cat tat aag ctg tcg cag 221
352 Asp Asn Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln
353 10          15          20          25
355 agg ggc tac gag tgg gat gcg gga gat gtg ggc gcc gcg ccc ccg ggg 269
356 Arg Gly Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly
357          30          35          40
359 gcc gcc ccc gca ccg ggc atc ttc tcc tcc cag ccc ggg cac acg ccc 317
360 Ala Ala Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro
361          45          50          55
363 cat cca gcc gca tcc cgc gac ccg gtc gcc agg acc tcg ccg ctg cag 365
364 His Pro Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln
365          60          65          70
367 acc ccg gct gcc ccc ggc gcc gcc gcg ggg cct gcg ctc agc ccg gtg 413
368 Thr Pro Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val
369          75          80          85
371 cca cct gtg gtc cac ctg gcc ctc cgc caa gcc ggc gac gac ttc tcc 461
372 Pro Pro Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser
373 90          95          100          105
375 cgc cgc tac cgc ggc gac ttc gcc gag atg tcc agc cag ctg cac ctg 509
376 Arg Arg Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu
377          110          115          120
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380 Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu
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VERIFICATION SUMMARY

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